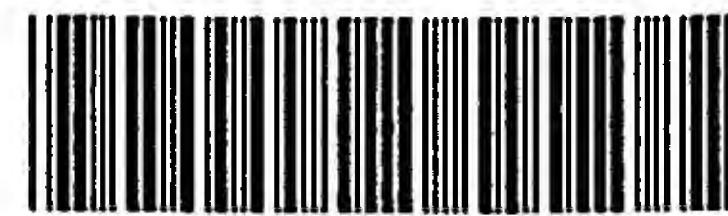# RAW SEQUENCE LISTING

re-run

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _09/943,443_

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 1 <110> APPLICANT: ANDERSEN, Peter
 2         NIELSEN, Rikke
 3         OETTINGER, Thomas
 4         RASMUSSEN, Peter Birk
 5         ROSENKRANDS, Ida
 6         WELDINGH, Karin
 7         FLORIO, Walter
 8 <120> TITLE OF INVENTION: NUCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS
 9         DERIVED FROM M. TUBERCULOSIS
10 <130> FILE REFERENCE: 670001-2002.1
11 <140> CURRENT APPLICATION NUMBER: US 09/943,443
12 <141> CURRENT FILING DATE: 2001-08-30
13 <150> PRIOR APPLICATION NUMBER: US/09/050,739
14 <151> PRIOR FILING DATE: 1998-03-30
15 <150> PRIOR APPLICATION NUMBER: 0376/97
16 <151> PRIOR FILING DATE: 1997-04-02
17 <150> PRIOR APPLICATION NUMBER: 1277/97
18 <151> PRIOR FILING DATE: 1997-11-10
19 <150> PRIOR APPLICATION NUMBER: 60/044,624
20 <151> PRIOR FILING DATE: 1997-04-18
21 <150> PRIOR APPLICATION NUMBER: 60/070,488
22 <151> PRIOR FILING DATE: 1998-01-05
23 <160> NUMBER OF SEQ ID NOS: 173
24 <170> SOFTWARE: PatentIn Ver. 2.0
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27 <211> LENGTH: 381
28 <212> TYPE: DNA
29 <213> ORGANISM: Mycobacterium tuberculosis
30 <400> SEQUENCE: 1
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32      atcgaaccct gctgaccgag aggacttgtg atgtcgcaaa tcatgtacaa ctaccccgcg 120
33      atgttgggtc acgccgggga tatggccgga tatgccggca cgctgcagag cttgggtgcc 180
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35      tatcaggcgt ggcaggcaca gtggaaccag gccatggaag atttggtgcg ggcctatcat 300
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37      gccgccaaat ggggcggcta g                                         381
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40 <211> LENGTH: 96
41 <212> TYPE: PRT
42 <213> ORGANISM: Mycobacterium tuberculosis
43 <400> SEQUENCE: 2
44      Met Ser Gln Ile Met Tyr Asn Tyr Pro Ala Met Leu Gly His Ala Gly
45        1               5                  10                  15
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RAW SEQUENCE LISTING   DATE: 12/23/2008
PATENT APPLICATION: US/09/943,443   TIME: 16:32:02

Input Set : A:\09943443.raw
Output Set: N:\CRF4\12232008\I943443.raw

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46        Asp Met Ala Gly Tyr Ala Gly Thr Leu Gln Ser Leu Gly Ala Glu Ile
47                    20              25              30
48        Ala Val Glu Gln Ala Ala Leu Gln Ser Ala Trp Gln Gly Asp Thr Gly
49                    35              40              45
50        Ile Thr Tyr Gln Ala Trp Gln Ala Gln Trp Asn Gln Ala Met Glu Asp
51              50              55              60
52        Leu Val Arg Ala Tyr His Ala Met Ser Ser Thr His Glu Ala Asn Thr
53           65              70              75              80
54        Met Ala Met Met Ala Arg Asp Thr Ala Glu Ala Ala Lys Trp Gly Gly
55                        85              90              95
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58 <211> LENGTH: 467
59 <212> TYPE: DNA
60 <213> ORGANISM: Mycobacterium tuberculosis
61 <400> SEQUENCE: 3
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63        gcgacggcgt cataaacccg gacggcacct tgttggcggg ccccgcggtg ctgacgcccg 120
64        acgagtacaa ctcccggctg gtggccgccg acccggagtc caccgcggcg ttgcccgacg 180
65        gcgccgggct ggtcgttctg gatggcaccg tcactgccga actcgaagcc gagggctggg 240
66        ccaaagatcg catccgcgaa ctgcaagagc tgcgtaagtc gaccgggctg gacgtttccg 300
67        accgcatccg ggtggtgatg tcggtgcctg cggaacgcga agactgggcg cgcacccatc 360
68        gcgacctcat tgccggagaa atcttggcta ccgacttcga attcgccgac ctcgccgatg 420
69        gtgtggccat cggcgacggc gtgcgggtaa gcatcgaaaa gacctga 467
71 <210> SEQ ID NO: 4
72 <211> LENGTH: 108
73 <212> TYPE: PRT
74 <213> ORGANISM: Mycobacterium tuberculosis
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78        Leu Val Val Leu Asp Gly Thr Val Thr Ala Glu Leu Glu Ala Glu Gly
79                    20              25              30
80        Trp Ala Lys Asp Arg Ile Arg Glu Leu Gln Glu Leu Arg Lys Ser Thr
81                    35              40              45
82        Gly Leu Asp Val Ser Asp Arg Ile Arg Val Val Met Ser Val Pro Ala
83              50              55              60
84        Glu Arg Glu Asp Trp Ala Arg Thr His Arg Asp Leu Ile Ala Gly Glu
85           65              70              75              80
86        Ile Leu Ala Thr Asp Phe Glu Phe Ala Asp Leu Ala Asp Gly Val Ala
87                        85              90              95
88        Ile Gly Asp Gly Val Arg Val Ser Ile Glu Lys Thr
89                    100             105
91 <210> SEQ ID NO: 5
92 <211> LENGTH: 889
93 <212> TYPE: DNA
94 <213> ORGANISM: Mycobacterium tuberculosis
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96        cgggtctgca cggatccggg ccgggcaggg caatcgagcc tgggatccgc tggggtgcgc 60
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 98        taataggcgg taaagagtag cgggaagccg gccgaacgac tcggtcagac aacgccacag 180
 99        cggccagtga ggagcagcgg gtgacggaca tgaacccgga tattgagaag gaccagacct 240
100        ccgatgaagt cacggtagag acgacctccg tcttccgcgc agacttcctc agcgagctgg 300
101        acgctcctgc gcaagcgggt acggagagcg cggtctccgg ggtggaaggg ctcccgccgg 360
102        gctcggcgtt gctggtagtc aaacgaggcc ccaacgccgg gtcccggttc ctactcgacc 420
103        aagccatcac gtcggctggt cggcatcccg acagcgacat atttctcgac gacgtgaccg 480
104        tgagccgtcg ccatgctgaa ttccggttgg aaaacaacga attcaatgtc gtcgatgtcg 540
105        ggagtctcaa cggcacctac gtcaaccgcg agcccgtgga ttcggcggtg ctggcgaacg 600
106        gcgacgaggt ccagatcggc aagttccggt tggtgttctt gaccggaccc aagcaaggcg 660
107        aggatgacgg gagtaccggg ggcccgtgag cgcacccgat agccccgcgc tggccgggat 720
108        gtcgatcggg gcggtcctcg acctgctacg accggatttt cctgatgtca ccatctccaa 780
109        gattcgattc ttggaggctg agggtctggt gacgccccgg cgggcctcat cggggtatcg 840
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113  <211> LENGTH: 162
114  <212> TYPE: PRT
115  <213> ORGANISM: Mycobacterium tuberculosis
116  <400> SEQUENCE: 6
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119        Val Thr Val Glu Thr Thr Ser Val Phe Arg Ala Asp Phe Leu Ser Glu
120                       20                  25                  30
121        Leu Asp Ala Pro Ala Gln Ala Gly Thr Glu Ser Ala Val Ser Gly Val
122                   35                  40                  45
123        Glu Gly Leu Pro Pro Gly Ser Ala Leu Leu Val Val Lys Arg Gly Pro
124               50                  55                  60
125        Asn Ala Gly Ser Arg Phe Leu Leu Asp Gln Ala Ile Thr Ser Ala Gly
126           65                  70                  75                  80
127        Arg His Pro Asp Ser Asp Ile Phe Leu Asp Asp Val Thr Val Ser Arg
128                           85                  90                  95
129        Arg His Ala Glu Phe Arg Leu Glu Asn Asn Glu Phe Asn Val Val Asp
130                       100                 105                 110
131        Val Gly Ser Leu Asn Gly Thr Tyr Val Asn Arg Glu Pro Val Asp Ser
132                       115                 120                 125
133        Ala Val Leu Ala Asn Gly Asp Glu Val Gln Ile Gly Lys Phe Arg Leu
134               130                 135                 140
135        Val Phe Leu Thr Gly Pro Lys Gln Gly Glu Asp Asp Gly Ser Thr Gly
136           145                 150                 155                 160
137        Gly Pro
139  <210> SEQ ID NO: 7
140  <211> LENGTH: 898
141  <212> TYPE: DNA
142  <213> ORGANISM: Mycobacterium tuberculosis
143  <400> SEQUENCE: 7
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145        ataaccactc ttcgcgccat gaatgccagt gttggccagg cgctggcctg cgtccacgc 120
146        cacacaccgc acagattagg acacgccggc ggcgcagccc tgcccgaaag accgtgcacc 180
147        ggtcttggca gactgtgccc atggcacaga taaccctgcg aggaaacgcg atcaataccg 240
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149        tgggggtgat cagcagcgac cagttccggg gtaagtccgt gttgctgaac atctttccat 360
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152        gcgccgaggg caccgaaaac gtcatgcccg cgtcggcatt ccgggacagc ttcggcgagg 540
153        attacggcgt gaccatcgcc gacgggccga tggccgggct gctcgcccgc gcaatcgtgg 600
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155        ccaactacga agcggcgctg gccgcgctgg gcgcctaggc tttcacaagc cccgcgcgtt 720
156        cggcgagcag cgcacgattt cgagcgctgc tcccgaaaag cgcctcggtg gtcttggccc 780
157        ggcggtaata caggtgcagg tcgtgctccc acgtgaaggc gatggcaccg tggatctgaa 840
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162 <212> TYPE: PRT
163 <213> ORGANISM: Mycobacterium tuberculosis
164 <400> SEQUENCE: 8

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167    Leu Pro Ala Val Gly Ser Pro Ala Pro Ala Phe Thr Leu Thr Gly Gly
168                   20                  25                  30
169    Asp Leu Gly Val Ile Ser Ser Asp Gln Phe Arg Gly Lys Ser Val Leu
170                   35                  40                  45
171    Leu Asn Ile Phe Pro Ser Val Asp Thr Pro Val Cys Ala Thr Ser Val
172               50                  55                  60
173    Arg Thr Phe Asp Glu Arg Ala Ala Ala Ser Gly Ala Thr Val Leu Cys
174     65                  70                  75                  80
175    Val Ser Lys Asp Leu Pro Phe Ala Gln Lys Arg Phe Cys Gly Ala Glu
176                   85                  90                  95
177    Gly Thr Glu Asn Val Met Pro Ala Ser Ala Phe Arg Asp Ser Phe Gly
178                  100                 105                 110
179    Glu Asp Tyr Gly Val Thr Ile Ala Asp Gly Pro Met Ala Gly Leu Leu
180                  115                 120                 125
181    Ala Arg Ala Ile Val Val Ile Gly Ala Asp Gly Asn Val Ala Tyr Thr
182              130                 135                 140
183    Glu Leu Val Pro Glu Ile Ala Gln Glu Pro Asn Tyr Glu Ala Ala Leu
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185    Ala Ala Leu Gly Ala
186                  165
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191 <213> ORGANISM: Mycobacterium tuberculosis
192 <400> SEQUENCE: 9

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195        gggcgccgac gacgtgaggc acgtcatgtc tcagcggccc accgccacct cggtcgccgg 180
196        cagtatgtca gcatgtcag atgactccac gcagccttgt tcgcatcgtt ggtgtcgtgg 240
197        ttgcgacgac cttggcgctg gtgagcgcac ccgccggcgg tcgtccgcg catgcggatc 300
198        cgtgttcgga catcgcggtc gttttcgctc gcggcacgca tcaggcttct ggtcttggcg 360
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200        tctacgcggt gaactaccca gcaagcgacg actaccgcgc gagcgcgtca aacggttccg  480
201        atgatgcgag cgcccacatc cagcgcaccg tcgccagctg cccgaacacc aggattgtgc  540
202        ttggtggcta ttcgcagggt gcgacggtca tcgatttgtc cacctcggcg atgccgcccg  600
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204        gcatgttgtg gggcggcggg tcgttgccga caatcggtcc gctgtatagc tctaagacca  720
205        taaacttgtg tgctcccgac gatccaatat gcaccggagg cggcaatatt atggcgcatg  780
206        tttcgtatgt tcagtcgggg atgacaagcc aggcggcgac attcgcggcg aacaggctcg  840
207        atcacgccgg atgatcaaag actgttgtcc ctataccgct ggggctgtag tcgatgtaca  900
208        ccggctggaa tctgaagggc aagaacccgg tattcatcag gccggatgaa atgacggtcg  960
209        ggcggtaatc gtttgtgttg aacgcgtaga gccgatcacc gccggggctg gtgtagacct 1020
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213  <211> LENGTH: 217
214  <212> TYPE: PRT
215  <213> ORGANISM: Mycobacterium tuberculosis
216  <400> SEQUENCE: 10
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218         1               5                  10                  15
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220                         20                  25                  30
221        Asp Pro Cys Ser Asp Ile Ala Val Val Phe Ala Arg Gly Thr His Gln
222                 35                  40                  45
223        Ala Ser Gly Leu Gly Asp Val Gly Glu Ala Phe Val Asp Ser Leu Thr
224             50                  55                  60
225        Ser Gln Val Gly Gly Arg Ser Ile Gly Val Tyr Ala Val Asn Tyr Pro
226         65                  70                  75                  80
227        Ala Ser Asp Asp Tyr Arg Ala Ser Ala Ser Asn Gly Ser Asp Asp Ala
228                         85                  90                  95
229        Ser Ala His Ile Gln Arg Thr Val Ala Ser Cys Pro Asn Thr Arg Ile
230                     100                 105                 110
231        Val Leu Gly Gly Tyr Ser Gln Gly Ala Thr Val Ile Asp Leu Ser Thr
232                 115                 120                 125
233        Ser Ala Met Pro Pro Ala Val Ala Asp His Val Ala Ala Val Ala Leu
234             130                 135                 140
235        Phe Gly Glu Pro Ser Ser Gly Phe Ser Ser Met Leu Trp Gly Gly Gly
236         145                 150                 155                 160
237        Ser Leu Pro Thr Ile Gly Pro Leu Tyr Ser Ser Lys Thr Ile Asn Leu
238                         165                 170                 175
239        Cys Ala Pro Asp Asp Pro Ile Cys Thr Gly Gly Gly Asn Ile Met Ala
240                     180                 185                 190
241        His Val Ser Tyr Val Gln Ser Gly Met Thr Ser Gln Ala Ala Thr Phe
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